

OM of: US-08-711-417C-165 to: PIR_71:* out_format : pfs
 Date: Aug 28, 2002 10:06 AM
 About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
 -MODE=framed_n2p.model -DEV=xlp
 -O=/cgn2_1/USPTO_Spool/6228611/runat_28082002_100210_13574/app_query.fasta_1.1639
 -DB=PIR_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000
 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000
 -GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
 -DEEXT=7.000 -START=1 -MATRIX=bloms62 -TRANS=human40.cdi
 -LIST=45 -LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
 -MINLEN=0 -MAXLEN=200000000 -USER=6228611 -CGNL1.213 -NCPU=6
 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPY
 -WAIT -THREADS=1

Search information block:
 Query: US-08-711-417C-165
 Query length: 1551
 Database: PIR_71:
 Database sequences: 283138
 Database length: 96089334
 Search time (sec): 98.600000

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
pir2:A56355	+ 2449.00	2899.19	4.1e-154	518	DNA-binding protein Ikaros form 1
pir2:B56229	+ 1938.50	2295.23	2.2e-120	427	lymphoid transcription factor 1
pir2:I59572	+ 1933.50	2289.22	4.7e-120	431	Ikaros DNA binding protein - mouse
pir2:A56229	+ 1607.00	1902.69	1.7e-98	392	lymphoid transcription factor 1
pir2:JE0288	+ 323.00	374.61	1.3e-13	671	Kruppel-type zinc finger protein
pir2:Z29294	+ 321.50	374.53	1.6e-13	553	finger protein zfp-37 - mouse
pir2:S51037	+ 321.00	372.18	1.8e-13	675	zinc-finger protein - African c
pir2:I46899	+ 311.00	360.84	8.2e-13	636	gene NK10 protein - mouse
pir2:S10245	+ 309.00	362.31	1.1e-12	411	finger protein, testis - mouse
pir2:S26823	+ 308.00	355.23	1.3e-12	803	zinc finger protein ZNF43 - hu
pir2:G02075	+ 307.00	356.68	1.5e-12	595	transcription repressor zinc fi
pir2:JH0500	+ 305.50	348.80	2.0e-12	1191	zinc finger protein ZNF91 - hu
pir2:A3073	+ 304.50	349.92	2.1e-12	519	transcription activator ZNF35 -
pir2:A40751	+ 304.00	354.92	2.3e-12	485	finger protein MZF1 - human
pir2:B32891	+ 303.50	351.74	2.6e-12	651	finger protein 2, placental - h
pir2:A29253	+ 303.50	350.40	2.6e-12	758	finger protein hunchback, fru
pir2:A32891	+ 301.00	352.46	3.6e-12	428	finger protein 1, placental - h
pir2:A37107	+ 298.50	346.82	5.4e-12	580	spermatogenesis protein Zfp-35
pir2:S00647	+ 298.00	348.10	5.7e-12	469	zinc finger protein ZNF135 - hu
pir2:S06556	+ 295.50	335.84	9.5e-12	1350	finger protein - African clawe
pir2:I39311	+ 294.50	344.53	9.6e-12	439	finger protein (clone XlcoF28)
pir2:I38599	+ 294.00	341.61	1.1e-11	572	Kruppel-type zinc finger protei
pir2:A48157	+ 291.00	342.42	1.6e-11	348	zinc finger protein ZNF134 - hu
pir2:S05447	+ 288.50	335.02	2.5e-11	576	renal transcription factor Kid-
pir2:I08674	+ 287.50	334.60	2.5e-11	604	finger protein glass - fruit fl
pir2:A34612	+ 286.50	335.15	2.8e-11	496	probable finger protein ZNF2p56
pir2:T14757	+ 286.00	331.11	3.4e-11	686	zinc finger protein ZNF7 - huma
pir2:I38598	+ 285.50	330.33	3.7e-11	701	hypothetical protein ZNF2p57C1
pir2:I37570	+ 285.00	331.26	3.9e-11	589	zinc finger protein ZNF132 - hu
pir2:I50620	+ 285.00	329.24	4.3e-11	693	zinc finger protein - human (fr
pir2:J05146	+ 284.50	324.02	5.0e-11	1173	procr2 - chicken (fragment)
pir2:A57785	+ 279.00	323.48	1.1e-10	594	arylphorin gene-specific bindin
pir2:S08686	+ 278.50	322.04	1.2e-10	654	finger protein ZNF133 - human
pir2:S05548	+ 278.00	322.47	1.2e-10	582	finger protein ZFP-36 - human
pir2:S03677	+ 277.50	318.91	1.4e-10	816	gap protein hunchback - fruit f
pir2:S68858	+ 276.50	323.39	1.5e-10	428	finger protein (clone mkr3) - m
pir2:B34612	+ 275.50	318.39	1.7e-10	707	finger protein - mouse
pir2:JH0501	+ 275.00	320.11	1.8e-10	543	zinc finger protein ZNF8 - huma
	+ 274.50	319.50	2.1e-10	509	zinc finger protein Ckr1 - chid

pir2:S47071 + 273.00 319.86 2.5e-10 399 i finger protein HZF3, Krueppe
 pir2:S60520 + 272.00 320.16 2.9e-10 337 i finger protein ZNF81.1 - hum
 pir2:S46593 + 271.00 310.20 3.8e-10 914 i finger protein AZF1, asparag
 pir2:S47073 + 269.50 310.37 4.6e-10 732 i finger protein HZF2, Krueppe
 pir2:B39240 + 268.00 313.75 5.4e-10 407 i finger protein mfg2 - mouse

seq_name: pir2:A56355
 seq_documentation_block:
 DNA-binding protein Ikaros form 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
 C/Accession: A56355
 R/Molnar, A.; Georgopoulos, K.
 Mol. Cell. Biol. 14, 8292-8303, 1994
 A/Title: The Ikaros gene encodes a family of functionally diverse zinc finger DNA-bin
 A/Reference number: A56355; MUID:95059058
 A/Accession: A56355
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-518 <MOL>
 C/Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
 C/Keywords: alternative splicing; DNA binding

alignment_scores:
 Quality: 2449.00 Length: 521
 Ratio: 4.928 Gaps: 6
 Percent Similarity: 95.393 Percent Identity: 89.827

alignment_block:
 US-08-711-417C-165 x A56355 ..
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 1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
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 51 CCCCCCTGTAGCGATACTCCAGATAGGCGGATGAGCCATGCCGATCC 100
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34
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 101 CCGAGGACCTCTCCACACCTCGGGAGGACAGCAAGCTCCAAAGAGTGAC 150
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 34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
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 151 AGAGTCCTGCCAGTATGTTAAAGTAGACACTCAGAGTGTATGAAGAGAA 200
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 51 ArgGlyMetAlaSerAsnValLysValGluThrGlnSerAspGluGluAs 67
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 201 TGGCGCTGCTGTGAATGAATGAGGGAAGAAATGTCGGGAGGATTTAGGAA 250
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 67 nGlyArgAlaCysGluMetAsnGlyGluGluCysAlaGluAspLeuArgW 84
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 251 TGCTTGATGCTCGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
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 84 etLeuAspAlaSerGlyGluLysMetAsnGlySerHisArgAspGlnGly 100
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 301 AGCTCGGCTTGTGCGGAGTTGAGGACATTCGACTTCTTAACGGAAACT 350
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 101 SerSerAlaLeuSerGlyValGlyGlyLeuArgLeuProAsnGlyLysLe 117
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 351 AAAGTGTGATATCTGGGATCATTTTTCATCGGGCCCAATGTCTCATGG 400
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 117 uLysCysAspIleCysGlyIleValCysIleGlyProAsnValLeuMetV 134
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 401 TTCACAAAAGAACCCACACTGGAGAACCGGCCCTTCAGTGCATCATGTC 450
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 134 alHisLysArgSerHisThrGlyGluArgPropheCysCysAsnGlnCys 150
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 451 GGGCGCTCTTACCCAGAGGCGACCTGCTCCGCGCATCATCAAGCTGCA 500
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151 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuHi 167
501 TTCGGGGAGAACCCCTCAAAATGCCACCTCTGCAACTACGCTCGCCGC 550
167 sSerGlyGluLysProPheLysCysHisLeuCySAsnTyAlaCySArgA 184
551 GGAGGAGGCCCTCACTGGCCCACTGAGGACGCACTCCGTTGGTAACT 600
184 rgArgaspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 200
601 CACAATATGGAATATGTGCCGAAGCTATAAACAGCAAGACTCTTTAGA 650
201 HisLysCysGlyTyrcysGlyArgSerTyLysGlnArgSerSerLeuGl 217
651 GGAACATAAAGACGCTGCCACAACTACTTGGAAAGCATGGCCCTCCGG 700
217 uGluHisLysGluArgCysHisAsnTyLysGluSerMetGlyLeuProG 234
701 GCACACTGTACCCAGTCATTAAGAGAAGAACTAAGCACACAGTCAAAATGGCA 750
234 ly...MetTyProValIleLysGluGluThrAsnHisAsnGluMetAla 249
751 GAAGACCTGTGCAAGATAGATCAGAGAGATCTCTCGTCTGGACAGACT 800
250 GluAspLeuCySlysIleGlyAlaGluArgSerLeuValLeuAspArgLe 266
801 AGCAAGTAATGTCCCAACAGTAAAGAGCTTAAGAGCTCTATGCTCAAAATTTCTTG 850
266 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeuG 283
851 GGGCAAGGGCCTGTCGGACACGCCCTTACACAGTGCACAGTACGACAGAAG 900
283 lyAspLysCysLeuSerAspMetProTyraSpSerAlaAsnTyGluLys 299
901 GAGAACGAAATGATGAAGTCCCAGCTGATGGCAGCAAGCCATCAACAACGC 950
300 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAsnAl 315
951 CATCAACTACTCTGGGGCCGAGTCCCTCGCCCGCTGGTGCAGACGCCCC 1000
315 alLeAsnTyLysGluAlaGluSerLeuArgProLeuValGlnThrProp 332
1001 CGGGCGGTCCGAGGTGGTCCCGGTATCATAGCCGGATGTACACAGCTGCAC 1050
332 roGlySerSerGluValValProValIleSerSerMetTyGlnLeuHis 348
1051 AGG...CGCTCGAGGCGACCCCGCTCTCAACCACTCGCCGCCAGACAG 1097
349 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnasp... 364
1098 CGCGTGAGGTACCTGTGCTGTCTCTCCAAGGCCAAGTTGGTGCCTCGG 1147
365 AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 381
1148 AGCGGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGGAG 1197
381 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 397
1198 AGCAACAACGAGGAGCAGCGACGGCGTCTTATCTACCTGACCAACACAT 1247
398 SerAsnAlaGluGluGlnArgSerGlyLeuIleTyLysLeuThrAsnHisI 414
1248 CGCCCGAGCGCGCAACGC...GTGTGCTCTAAGGAGGAGCAGCAGCGCCT 1294
414 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGluGlnArgAla 431
1295 AGCACTCTGTCGCGCGCCCTCCGAGAACTCGCAGGACGGCGCTCCGCGTG 1344
431 TyGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 447
1345 GTCACACACAGCGGGAGCAGATGAAGGTGTACAGTGCAGAACACTCGCG 1394
448 ValSerThrSerGlyGluGluLeuLysValTyrcysGluHisCysArg 464

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1395 GGTGCTCTTCTTCGGATCAGCTCATGTACACCATCCACATG.....G 1435
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alignment_scores:
  Quality: 1938.50      Length: 518
  Ratio: 4.728          Gaps: 7
  Percent Similarity: 79.151  Percent Identity: 73.745

alignment_block:
  US-08-711-417C-165 x B56229 ..
  Align seq 1/1 to: B56229 from: 1 to: 437

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51  CCCCCCTGTAAAGGATACTCCAAGATGAGGGGGATGAGCCCATGCCGATCC  100
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17  rProProValSerAspThrProAspGluGlyAspGluProMetProValP  34
101  CCAGGAGCCTCTCCACACCTCGGAGGACAGCAAAGCTCCAAGAGTGAC  150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerasp  50
151  AGAGTCGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGATGAAGAA  200
|||:|:|
51  ArgGlyMet..... 53
201  TGGGCGGTGCCTGTGAATGAATGGGGAAGAATGTCCGGAGGATTACGAA  250
53  ..... 53
251  TGCTTGATGCCTCGGAGAGAAATGAATGCGTCCACACAGGACCACGAGC  300
53  ..... 53
301  AGCTCGCTTTGTTCGGAGTTTGAGGCAATTCGACTTCCTAACCGGAAAACT  350

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53 ..... 53
351 AAAGTGTGATATCTGTGGGATCATTTTGCATCGGGCCCAATGTCTCATGG 400
53 ..... 53
401 TTCACAAAAGAACCCACACTGGAGACGGCCCTTCAGTGCATCAATCAGTGC 450
54 ..... 53
451 GGGCCCTCAATTCACCAAGGAGGCAACCTGCTCCGGSCACATCAAGCTGCA 500
64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuAurGHisLleLysLeuHi 80
501 TTCGGGGAGAACCCCTCAATGCCACCTCTGCAACTACGCTGCCGCC 550
80 SSeRGlyGluLysProPheLysCysHisLeuCysAsnTyrAlaCysAra 97
551 GGAGGACGCCCTCACTAGCCCACTGAGGACGACCTCCGTTGGTAAACCT 600
97 rGArgAspAlaLeuThrGlyHisLeuAurGThrHisSerValGlyLysPro 113
601 CACAAATGTGGATATGTGGCCGAGCTATTAACAGCGAAGCTCTTTAGA 650
114 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeuGl 130
651 GGAACATAAAGAGCGCTGCCCAACTACTTGGAAAGCATGGCCCTCCGG 700
130 uGluHisLysGluAurGysHisAsnTyrLeuGluSerMetGlyLeuPro 147
701 GCACACTGTACCCAGCTCATTAAGAAGAACTAAGCACAGTGAATGGCA 750
147 ly...MetTyrProValLleLysGluLThrAsnHisAsnGluMetAla 162
751 GAAGACCTGTGCAAGATAGGATCAGAGATCTCTGCTGTCGACAGACT 800
163 GluAspLeuLysLysLleGlyAlaGluArgSerLeuValLeuAspArgLe 179
801 AGCAAGTATGTGCGCAACCTAAGAGCTCTATGCTTCAGAAATTTCTTG 850
179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeu. 195
851 GGGCAACAGGGCTGTCCGACACGCCCTACGACAGTCCAGCTGACGAGAG 900
196 ..AspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 211
901 GAGAACGAAATGATGAAGTCCCGATGATGACCAAGCCATCAACAACGC 950
212 Glu...AspMetMetThrSerHisValMetAspGluAlaLleAsnAl 227
951 CATCAACTTACCTGGGGCGGAGTCCCTGCGCCCGCTGGTGCGACGCCCC 1000
227 alLeAsnTyrLeuGlyAlaGluSerLeuAurGProLeuValGlnThrPro 244
1001 CGGCGGTTCGAGGTGGTCCCGGTTCATCAGCCCGATGTACGAGCTGAC 1050
244 roGlySerSerGluValValProValLleSerSerMetTyrGlnLeuHis 260
1051 AGG...CGCTCGGAGGCGACCCCGCGCTCCACCACTCGGCCCGAGACAG 1097
261 LysProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp... 276
1098 CGCGGTGGAGTACTGTCTGCTCTCCCAAGGCCAAGTTGGTGGCCCTCGG 1147
277 .AlaValAspAsnLeuLeuLeuSerLysAlaLysSerValSerSerG 293
1148 AGCGGAGGCGTCCCGAGCACAGCTGCCAAGACTCCACGCGACACCGAG 1197
293 luArgGluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 309
1198 AGCAACAACAGGAGGAGCGACGCGCTCTTACTACCTGACCAACACAT 1247
310 SerAsnAlaGluGlnArgSerGlyLleTyrLeuThrAsnHisIl 326

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1248 CGCCCGAGCGCGCAACGC...GTGTGCTCAAGGAGGAGCACCAGCGCT 1294
326 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAlaT 343
1295 ACGACCTGTGCGCGCGCTCCGAACTCGAGAACTCGAGACGCGCTCCGCTG 1344
343 yTGLuValLeuArgAlaLleSerGluAsnSerGlnAspAlaPheArgVal 359
1345 GTCAGACCAAGCGGGAGCAGATGAAGGTGTACAAGTGCGAACACTGCCG 1394
360 ValSerThrSerGlyGluGlnLeuLysValTyrLysCysGluHisCysAr 376
1395 GTGCTCTTCTTCTGATCAGCTCATGTACACCATCCACATGGGCTGCCACG 1444
376 gValLeuPheLeuAspHisValMetTyrThrLleHisMetGlyCysHisG 393
1445 GCTTCGCTGATCTTTTGTAGTCAACATGTGCGCTACACAGCAGCAGAC 1494
393 lyPheArgAspProPheGluCysAsnMetCysGlyTyrHisSerGlnAsp 409
1495 CGGTACGAGTTCTCTGTCGCACATTAACGCGAGGAGCACCCTTCCACAT 1544
410 ArGTYrGluPheSerSerHisLleThrArgGlyGluHisArgTyrHisLe 426
1545 GAGC 1548
426 uSer 427

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seq_name: pir2:I59572

seq_documentation_block:

Ikaros DNA binding protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 01-Dec-2000

C:Accession: I59572

R:Georgopoulos, K.; Moore, D.D.; Derfler, B.

Science 258, 808-812, 1992

A:Title: Ikaros, an early lymphoid-specific transcription factor and a putative media

A:Reference number: I59572; MUID:93068267

A:Accession: I59572

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-431 <RES>

A:Cross-references: GB:L03547; NID:g198286; PIDN:AAA66193.1; PID:g198287

C:Gene: Ikaros

C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

alignment_scores:

Quality: 1933.50 Length: 521

Ratio: 4.716 Gaps: 7

Percent Similarity: 78.695 Percent Identity: 73.321

alignment_block:

US-08-711-417C-165 x I59572

Align seg 1/1 to: I59572 from: 1 to: 431

1 ATGGATGCTGACGAGGTCAAGACATGTCTTCTCATCAGGGAAGAAAG 50

1 MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17

51 CCCCCCTGTAAAGCGTACTCCAGATGAGGCGCATGAGCCCATGCCGATCC 100

17 rProProValSerAspThrProAspGluGlyAspGluProMetProValP 34

101 CCAGGAGCCTCTCCACCACTCGGAGGACACAGCAAGCTCCCAAGATGAC 150

34 roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50

151 AGAGTGTGGCCAGTAATGTTAAAGTAGAGACTCAGAGTGTGAAGAGAA 200

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262 LysProProSerAspGlyProProArgSerAsnHisSerAlaGlnAsp.. 277
1098 CGCGTGGAGTACGTGCTGCTCTCCAGGCAAGTTGTCCTCGG 1147
278 .AlaValAspAsnLeuLeuSerLysAlaLysSerValSerSerg 294
1148 AGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAG 1197
294 luArggluAlaSerProSerAsnSerCysGlnAspSerThrAspThrGlu 310
1198 AGCAACAACGAGGAGCGAGCGGCTTATCTACCTGACCAACACCAT 1247
311 SerAsnAlaGluGlnArgSerGlyLeuIleTyrLeuThrAsnHisI 327
1248 CGCGGAGGCGGCAACGC...GTGCTGCTCAAGGAGGAGCAGCGCGCT 1294
327 eAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlnArgAla 344
1295 AGACCTGCTGCGCGCCCTCCGAGAACTCGAGGAGCGGCTCCGCGTG 1344
344 yrGluValLeuArgAlaAlaSerGluAsnSerGlnAspAlaPheArgVal 360
1345 GTCAGCACCAGCGGAGCAGATGAAGTGTACAAGTCCGAACACACTGCCG 1394
361 ValSerThrSerGlyGlnLeuLysValTyrLysCysGluHisCysAr 377
1395 GGTGCTCTTCCTGGATCAGCTATGATCACCATCCACATG.....G 1435
377 gValLeuPheLeuAspHisValMetTyrThrIleHisMetGlyCysHisG 394
1436 GCTGCCACCGCTTCCGTGATCTTTGAGTCAACATGTGGGCTACAC 1485
394 lyCysHisGlyPheArgAspPropheGluCysAsnMetCysGlyTyrHis 410
1486 AGCAGGAGCGGTACGAGTCTCTGCGACATACGCGAGGAGGACCG 1535
411 SerGlnAspArgTyrGluPheSerSerHisIleThrArgGlyGluHisAr 427
1536 CTTCCACATGAGC 1548
427 gTyrHisLeuSer 431
seq_name: pir2:A56229

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seq_documentation_block:
Lymphoid transcription factor Ikaros/LyF-1, form IV - mouse
N;Alternate names: Ikaros/LyF-1 form I; Ikaros/LyF-1 form II; Ikaros/LyF-1 form III
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 01-Dec-2000
C;Accession: A56229
R;Hahn, K.; Ernst, P.; Lo, K.; Kim, G.S.; Turck, C.; Smale, S.T.
Mol. Cell. Biol. 14, 7111-7123, 1994
A;Title: The lymphoid transcription factor LyF-1 is encoded by specific, alternative
A;Reference number: A56229; M0ID:95021239
A;Accession: A56229
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-392 <HAH>
A;Cross-references: GB:S74517
C;Superfamily: zinc finger protein 2FP-36; LIM metal-binding repeat homology
C;Keywords: alternative splicing

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alignment_scores:
Quality: 1607.00 Length: 538
Ratio: 4.514 Gaps: 7
Percent Similarity: 66.171 Percent Identity: 61.710

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alignment_block:

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US-08-711-417c-165 x A56229 ..
Align seg 1/1 to: A56229 from: 1 to: 392

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111 :::
51 ArgGlyMet..... 53
201 TGGGGCTGCTGTAATGAATGGGAAGAATGTGGAGGATTTACGAA 250
53 ..... 53
251 TGGTTGATCCCTCGGAGAGAAATGAATGCTCCACAGGACCAAGGC 300
53 ..... 53
301 AGCTCGCTTTTGTGGGAGTTGGAGCATTCGACTTCTTAACGAAACT 350
53 ..... 53
351 AAAGTGTGATATCTGTGGGATCATTTGGCATCGGGCCCAATGTGCTCATGG 400
53 ..... 53
401 TTCAAAAAGAGACACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGC 450
54 .....GlyGluArgProPheGlnCysAsnGlnCys 63
451 GGGGCTCATTCACCAGAGGCAACCTGCTCCGGCAGCATCAAGCTGCA 500
64 GlyAlaSerPheThrGlnLysGlyAsnLeuLeuArgHisIleLysLeuH 80
501 TTCCGGGAGAACCCCTTCAAAATGCCACCTCTGCAACTACGCTCCGCC 550
80 sSerGlyLysProPheLysCysHisLeuCysAsnTyrAlaCysArgA 97
551 GGAGGAGCGCCCTACTGGCCACTCAGACGCGACTCCGTTGGTAAACT 600
97 rgArgAspAlaLeuThrGlyHisLeuArgThrHisSerValGlyLysPro 113
601 CACAAATGTGATATTGTGGCCGAAGCTATAAAGACGCAACGCTCTTTAGA 650
114 HisLysCysGlyTyrCysGlyArgSerTyrLysGlnArgSerSerLeu 130
651 GGAACATAAGAGCGCTGCCACAACTACTTGGAAAGCATGGCGCTCCGG 700
130 uGluHisLysGluArgCysHisAsnTyrLeuGluSerMetGlyLeuPro 147
701 GCACACTGTACCCAGTCAATTAAGAAAGAACTAAGCAGACAGTGAATGGCA 750
147 ly...ValCysProValIleLysGluThrAsnHisAsnGluMetAla 162
751 GAAGACCTGTGCAAGATAGATCAGAGATCTCTGCTGTCGACAGACT 800
163 GluAspLeuCysLysIleGlyAlaGluArgSerLeuValLeuAspArgLe 179
801 AGCAAGTAAATGTCGCCAAACCTAAGAGCTCTATGCTCCAGAAATTTCTTG 850
179 uAlaSerAsnValAlaLysArgLysSerSerMetProGlnLysPheLeu 196
851 GGCACAAAGGCGCTGCCAGACCGCCTACGACAGTGCCTACGAGAGAG 900
196 lyAspLysCysLeuSerAspMetProTyrAspSerAlaAsnTyrGluLys 212
901 GAGAACGAATGATGAAGTCCCGCTGATGACCAAGCCATCAACACGC 950
213 Glu...AspMetMetThrSerHisValMetAspGlnAlaIleAsnAl 228
951 CATCAACTACCTGGGGCGAGTCCCTCGCGCGCTGCTGTCAGACGCCCC 1000
228 alIeAsnTyrLeuGlyAlaGluSerLeuArgProLeuValGlnThrProp 245
1001 CGGGCGGTTCCGAGTGTGTCGGGTATCATCGCCGATGTACCACTGCAC 1050
245 roGlySerSerGluValValProValIleSerSerMetTyrGlnLeuHis 261
1051 AGG...CGTCCGAGGACCGCCCGCTCCCAACCACTCGGCCAGGACAG 1097
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1  ATGATGCTGACGAGGCTCAAGACATGCTCTTCTCATCATCAGGGAAGAAAG 50
1  MetAspValAspGluGlyGlnAspMetSerGlnValSerGlyLysGluSe 17
51  CCCCCTGTAAAGGATACCTCCAGATGAGGCGGATGAGCCCATGCCATCC 100
17  rProProValSerAspThrProAspGluGlyAspGluProMetProValp 34
101  CCGAGGACCTCTCCACACCTCCGGGAGGAGCAGCAAAAGCTCCAGAGTGAC 150
34  roGluAspLeuSerThrThrSerGlyAlaGlnGlnAsnSerLysSerAsp 50
151  AGA...GTCGTGGCC..... 162
51  ArgGlyMetValAlaIatyrGlyAlaAspGlyPheArgAspPheHisAlaI 67
163  .....AGTAATGTTAAAGTAGACTCAGAGTG 190
67  eIleSerAspArgGlyMetProSerAsnValLysValGluThrGlnSerA 84
191  ATGAAGAGATGGCGCTGCTGTAATGAATGGGGAAGAANTGTGCGGAG 240
84  spGluAsnGlyArgAlaCysGluMetCasnGlyGluGluCysAlaGlu 100
241  GATTTACGAATGCTTGATGCTCGGAGAGAAAAATGAATGGCTCCACAG 290
101  AspLeuArgMetLeuAspAlaSerGlyGluLysMetAsnGlySerHisAr 117
291  GGACCAAGCAGCTCGGCTTTGCGGAGTTGGAGCATTCGACTTCCTA 340
117  gAspGlnGlySerSerAlaLeuSerGlyValGlyGlyIleArgLeuProA 134
341  ACGGAAACTAAAGTGTGATATCTGCGGATCATTTGCATCGGGCCCAAT 390
134  snGlyLysLeuLysCysAspIleCysGlyIleValCysIleGlyProAsn 150
391  GTGCTCATGTTACAAAAAGACCCACACTGGAGAACGGCCCTCCAGTG 440
151  ValLeuMetValHisLysArgSerHisThr..... 160
441  CAATCAGTCGGGGCCCTCATTCACCCAGAGAGGCAACCTGTCGGGCACA 490
160  ..... 160
491  TCAAGTGCATTCGGGGAGAGACCCCTTCAAATGCCACTCTGCAACTAC 540
160  ..... 160
541  GCCTGCCGGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGT 590
160  ..... 160
591  TGGTAAACCTCACAATGTGGATATTGTGGCGGAAGCTATAACAGCGAA 640
160  ..... 160
641  CGTCTTTAGAGAACATAAAGAGCGCTGCCAACACTACTTGGAAAGCATG 690
160  ..... 160
691  GGCCTTCGGGCACACTGTACCAGTCAATTAAAGAAACTAAGACAG 740
160  ..... 160
741  TGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGATCTCTCGTCG 790
160  ..... 160
791  TGGACAGACTAGCAAGTAATGTGCGCAAAACGTAAGAGCTCTATGCCTCAG 840
160  ..... 160
841  AAATTTCTGGGGACAGGGGCTGTCCGACACAGCCCTACGACAGTGCCAC 890

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161  .....AspLysCysLeuSerAspMetProTyrAspSerAlaAs 173
891  GTACGAGAGGAGAGACAAATCATGAAGTCCACGTGATGACCAAGCCA 940
173  nTyrGluLysGlu...AspMetMetThrSerHisValMetAspGlnAlaI 189
941  TCAACACAGCCCATCAACTACCTGGGGCCGAGTCCCTGCGCCGCTGGTG 990
189  leAsnAsnAlaIleasnTyrLeuGlyAlaGluSerLeuArgProLeuVal 205
991  CAGAGCCCGCGGGGTTCCGAGGTGTCTCCGGTCAATCATCAGCCGATGTA 1040
206  GlnThrProProGlySerSerGluValValProValIleSerSerMetTy 222
1041  CCAGCTGCACAGG...CGCTCGGAGGCGACCCGCGCTCCCAACCACTCGG 1087
222  rGlnLeuHisLysProProSerAspGlyProProArgSerAsnHisSerA 239
1088  CCCAGGACAGCGCGGTGGAGTACCTGTGCTGTCTCCAAAGGCCAAGTTG 1137
239  laGlnAsp...AlaValAspAsnLeuLeuLeuSerLysAlaLysSer 254
1138  GTGCCCTCGGAGCGGCGGTCCCGAGCAACAGCTGCCAAGACTCCAC 1187
255  ValSerSerGluArgGluAlaSerProSerAsnSerCysGlnAspSerTh 271
1188  GGACACCGAGAGCAACACAGGAGCAGCGCGCTCTTATCTACCTGA 1237
271  rAspThrGluSerAsnAlaGluGluGlnArgSerGlyLeuIleTyrLeuT 288
1238  CCAACACATCGCCCGGAGCGCGCAACGC...GTGTCGCTCAAGGAGGAG 1284
288  hrAsnHisIleAsnProHisAlaArgAsnGlyLeuAlaLeuLysGluGlu 304
1285  CACCGCGCTACGACCTGCTGCGCGCGCTCCGAGAACTCGCAGGACGC 1334
305  GlnArgAlaTyrGluValLeuArgAlaAlaSerGlnAsnSerGlnAspAl 321
1335  GCTCCGGTGTGTACAGCACCGGGGAGCAGATGAAGTGTACAAGTGC 1384
321  aPheArgValValSerThrSerGlyGluGlnLeuLysValTyrLysCysG 338
1385  AACACTCGCGGTGCTCTTCTCGATCAGCTCATGTACACCATCCACATG 1434
338  luHisCysArgValLeuPheLeuAspHisValMetTyrThrIleHisMet 354
1435  GGCTGCCACGCTTCCGTGATCTTTTGTAGTGCAACATGTGCGGTACCA 1484
355  GlyCysHisGlyPheArgAspProPheGluCysAsnMetCysGlyTyrH 371
1485  CAGCCGAGCGGTACGAGTTCTCGTGGCACATAACGCGAGGGAGCAC 1534
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1535  GCTTCCACATGAGC 1548
388  rGyrHisLeuSer 392

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seq_name: pir2:JE0288

seq_documentation_block:

krueppel-type zinc finger protein - human

C:Species: Homo sapiens (man)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 01-Dec-2000

C:Accession: JE0288

R:Katoch, O.; Oguri, T.; Takahashi, T.; Takai, S.; Fujiwara, Y.; Watanabe, H.

Biochem. Biophys. Res. Commun. 249, 595-600, 1998

A:Title: ZK1, a novel krueppel-type zinc finger gene, is induced following exposure t

A:Reference number: JE0288; MUID:98401134

A:Accession: JE0288

A:Status: preliminary

A:Molecule type: mRNA

A; Residues: 1-671 <KAT>
C; Superfamily: zinc finger protein 2FP-36; LIM metal-binding repeat homology

alignment_scores:		
Quality:	323.00	Length: 550
Ratio:	1.166	Gaps: 21
Percent Similarity:	50.364	Percent Identity: 22.364

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alignment_block:
US-08-711-417C-165 x JE0288
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Align seq 1/1 to: JE0288 from: 1 to: 671

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73 GluSerLysAspGlyThrGlnCysGlyGluThrSerGlnIleGlnAsn 89
150 CAGAGTCGTGCCAGTAATGTAAAGTAGACACTCAGAGTCATGAAGA 199
| ::|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
89 pSerIleValThrLysAsnThrLeuProGlyValcylProCysGluSerS 106
200 ATGGCGCTGCCTGTAAGAATGAGGAAGAATGTGCGGAGATTTCAGA 249
::| |::|||: |||: |||: |||: |||: |||: |||: |||: |||:
106 erMetArgGlyGluLysValMetGlyHisSerSerLeuAsnCysTyri 122
250 ATGCTTGATGCTCG.....GGAGCAA 272
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123 ArgValGlyAlaGlyHisLysProHisGluThrHisGluCysGlyGlu 139
273 AATGAATGGCTCCACAGGAGCACAGGAGCTCG..... 306
| ::|||: |||: |||: |||: |||: |||: |||: |||: |||:
139 sProasp...ThrHisLysGlnArgGlyLysAlaPheSerTyHisAsn 155
306 306
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307GCTTTGCGGAGCTTGA..... 324
172 LysGluCysGlyLysSerPheSerSerLeuGlyAsnLeuGlnArgHisMe 188
325 ..GGCATTCGACTTCCTAACGGAAAACTAAAGTGCGATCTCTGGGATCA 373
talaValGlnargGlyAspGlyProTyLysCysLysLysCysGlyLysA 205
374 TTGCATCGGCCCAATGTGCTCATGTTGCACAAAAGAGCCACACTGGA 423
::| |::|||: |||: |||: |||: |||: |||: |||: |||: |||:
205 laPhePheTrpProSerLeuLeuHisMetHisGluArgThrHisThrGly 221
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222 GluLysProTyrgLuoCysLysGlnCysSerLysAlaPheSerPheTySe 238
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524 GCACCTCTGAACATACGCTCCCGGGAGGAGCCCTCACTGGCCAC 573
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255 ysLysGlnCysSerLysAlaPheProPheTySerSerTyLeuArgHis 271
574 CTGAGAGCGACACTCGTGGTAAAGCTCAAAATGTGGATATTTGGCCGC 623
|||||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
272 GluArgThrHisThrGlyGluLysProTyrgLysCysLysGlnCysSerLy 288
624 AGCTAT.....AAACAGCGAAGCTCTTAG 649
||||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
288 salaPheProAspSerSerCysLeuLeHisGluArgThrHisThrG 305
650 AGGAACATAAAGAGGCTGCCACAACACTACTTGGAAAGCATGGCCCTCCG 699
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305 lyeGluIseProTyrgChrcCysLysGlnCysGlyLysAlaPheIseValSer 321

700 GGCAACACTGTACCACCTCATTTAAAGAAGAAACTAAGCACAGTGAATGGC 749
|||||::||| ::::| ||||| |||||
322 GlySerLeuGln.....ArgHisThrThrHisSerAlaGluLys 335

750 AGAAGACCTGTGCAACATAGGATCAGAGAGATCTCTCGTGCTGGACAGAC 799
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335 sProTyraAlaCysGlnGlnCysGlyLysAlaPheHisHisLeuGlySerP 352

800 TAGCAAGTAATGTGCGCAACAGCTAAGAGCTCATGCTCCAGAAATTT... 846
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352 heGlnArgHisMetIleArgHisThrGlyAsnGlyProHisLysCysLys 368

847 CTTGGGCACAAGGCCCTGTCCGACACGCCCTACGACAGTCGCCACGTACGA 896
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369 IleCysGlyLysGlyPhe...AspCysProSerSerLeuGlnSerHisGl 384

897 GAGGAGAACGAATGATNAAGTCCCACGTGATGGACCAAGCCATCAACA 946
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384 uArgThrHisThrGlyGluLysProTyrgluCysLysGlnCys...GlyL 400

947 ACGCCATCAACTACCTGGGGCGGAGTCCCTCGCCCGCTGTGTGCAGAG 996
: |||||:: ||| ||| :::: | |||||
400 ysAlaLeuSerHisArgSerSerPheArgSerHisMetIleMethisThr 416

997 CCCCCGGGGCGTTCGGAG.....GTGGTCCC 1022
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417 GlyAspGlyProHisLysCysLysValCysGlyLysAlaPheValTyrrPr 433

1023 GGTCAATCAGCCGATGATACCAAGCTGCACAGCGCTCGGAGGCGACCCCG 1072
| ::: :||| |||||
433 oSerVal.....PheGlnArgHisGluArgThr..... 442

1073 GCTCCAACCACTGGCCCCAGGACAGCGCGTGGAGTAGTACCTGCTGCTGCTC 1122
|||||::||| :::: | |||
443HisThrAlaGlu.....IleProTyrr..... 449

1123 TCCAAAGGCCAAGTTGGTGCCCTCGGAGCGCGAGCGTCCCGGAGCAACAG 1172
|||||::||| :::: | |||
450 ...LysCysLysGlnCysGlyLysAlaTyraArgIleSerSerSerLeuar 465

1173 CTGCCAAGACTCCACGACACCGAGACAACAGGAGGAGCAGCGCAGCG 1222
||| |||||:: ||| :::: | |||
465 gArgHisGluThrThrHisThrGlyGluLysProTyrgluCysThrLeug 482

1223 GTCTATCTACCTG.....ACCAACCAC 1245
|| ::::: | |||||
482 lyLysAlaPheIleAspPheCysSerPheGlnAsnHisLysThrHis 498

1246 ATCGCCCGACGCGCGCAACGCGTCTCGCTCAAGGAGGAGCACC CGCCCTA 1295
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499 ThrGlyGluLysPro.....TyrgluCysLysGluCysGlyLysAlaph 513

1296 CGACCTGCTCGCGCGCGCTCCGAGAACTCGCAGGAGCGCGCTCGCGTGG 1345
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513 eSerArgPheArgtyrLeuSerArgHisLysArg..... 524

1346 TCAGCACACGCGGGGAGCAGATGAAGGTGTACAAGTCGCAACACTGCCGG 1395
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525 ...ThrHisThrGlyGlu.....LysProTyrgluCysLysThrCysArg 538

1396 GTGCTCTTTCCTGGATCAGCTCATGTACACCATCCACATGGGCTGCCACGG 1445
||| :::: | |||||
539 LysAlaPheGlyHisTyraSpAsnLeuLysValHisGluArgIleHisSe 555

1446 CTTCCGCTGATCCTTTTGAGTCCACATGTCCGGCTACACAGCAGGACC 1495
: :: :||| ||||| | |||||
555 rGlyGluLysProTyrgluCysLysGluCysGly.....Lysa 568

1496 GGTACGAGTTCTCGTCGCACATAACGGGAGGGGAGCACCCTCCACATG 1545
||| |||||:: ||| |||||
568 lApheSerTrpLeuThrCvsPheLeuArHigLgu...ArgIleHisMet 583


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495 luCysTyrGluCysGlyLysAlaPheAsnAlaLysSerGlnLeuValIle 511
1429 CACATGGGCTGCCAGCGCTCCGTTGATCCCTTTGAGTGCAACATGTCGG 1478
512 HisGlnArgSerHisThrGlyGluLysProTyrGluCysIleGluCysGI 528
1479 CTACCAGCCAGCAGCAGCGGTACGAGTCTCGTCGCACATA 1518
528 YLysAlaPheLysGlnAsnAlaSerLeuThrLysHisMet 541
seq_name: pir2:S51037

seq_documentation_block:
zinc-finger protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 01-Dec-2000
C:Accession: S51037; S06565
R:Schaefer, U.; Rausch, O.; Boumeester, T.; Pieler, T.
Eur. J. Biochem. 226, 567-576, 1994
A:Title: Sequence-specific recognition of a repetitive DNA element by a C(2)H(2) zinc-finger protein
A:Reference number: S51037; MUID:95094815
A:Accession: S51037
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-675 <SCH>
R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoechel, J.
Mol. Biol. 208, 639-659, 1989
A:Title: Second-order repeats in Xenopus laevis finger proteins.
A:Reference number: S05632; MUID:90040698
A:Accession: S06565
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 85-448, 'K', 450-613 <NIE>
A:Experimental source: clone XLCGF20-1
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C:Keywords: DNA binding; zinc finger

alignment_scores:
Quality: 321.00 Length: 616
Ratio: 1.092 Gaps: 21
Percent Similarity: 47.727 Percent Identity: 20.617

alignment_block:
US-08-711-417C-165 x S51037 ..
Align seg 1/1 to: S51037 from: 1 to: 675

82 GATGAGCCCATCGGATCCCGGAGGACCTCTCCACCACCTCG.....123
6 GluGluProTyrGluPheProGluAsnThrPheGlyThrAsnGluLeuLe 22
124 .GGAGGACACAAAGCTCCAAAGAGTACACAGAGTCGTGGCCAGTAAGTTA 172
22 uProAsnTyrGlnGluAsnCysThrAspGlyGluAlaIleSerAspThrL 39
173 AAGTAGAG.....ACTCAGAGTATGATGAG 198
39 ysSerAspLeuGluTyrLeuGluValGluIleThrAspAlaHisGluGlu 55
199 AATGGGGCTGCTGTAATGATGGGAGAGATGTGCGGAGATTACG 248
56 SerAsnThrAspLysProPheThrCysThrGluCysGlyLysThrPheTh 72
249 AATGCTTGATGCTCGGGAGAGAAATGAAT...GGCTCCACAGGAGACC 295
72 r.....ArgLysProAsnTyrGluSerHis.....80
296 AAGGACGCTCGGCTTGTCTGGGAGTTGGAGGATTCGACTTCTCAACGGA 345
81 .....IleArgAlaHisLysGly 86

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346 AAA.....CTAAAGTGTGATATCTGTGGATCATTTTCATCGGGCCCAA 389
87 GluLysProPheSerCysMetValCysAspLysAlaPheAlaTrpLysse 103
390 TGTGCTCATGTTTCACAAAAGCCACACCTGGAGACGGCCCTTCCAGT 439
103 rAsnLeuLeuValHisTyrSerValHisSerGlyGluLysProPheSerC 120
440 GCAATCAGTGGGGGCCCTATTCCACCAAGAGGCAACCTGCTCCGGCAC 489
120 ysThrGluCysAspLysThrPheSerAsnLysAlaGlnLeuGluLysHis 136
490 ATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTGCAACTA 539
137 LeuArgValHisThrGlyGluLysProTyrSerCysGluGlnCysGlyLy 153
540 GCGCTGCGCGCGGAGGAGCCCTCACTGGCCACCTGAGGAGCAGCCTCG 589
153 sSerPheAlaHisLysCysValLeuAspSerHisGlnArgThrHisThrG 170
590 TTGGTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCA 639
170 lyAspLysProPheSerCysThrGluCysGlyLysLysPheSerGlnArg 186
640 AGCTCTTTAGAGACATATAAGACGCG.....666
187 GlyAsnLeuHisLysHisLysThrHisLysLeuAspGlnProHisLe 203
667 .TGCCACAACCTACTTGGAAACATGGGCTTCCGGGACACACTGTACCCAG 715
203 ucysAlaGluCysGlyLysThrPheSerPheLysSerThrLeu.....217
716 TCATTAAAGAAAGAACTAAGCACAGTGAATG.....747
218 ..LeuGluHisGlnLysIleHisSerGluIleArgProLeuSerGluPhe 233
748 .....GCAGAGACCTGTGCAAG.....765
234 GlyLysThrPheSerAspAlaHisAsnLeuLysHisGlnSerThrPh 250
766 .....ATAG 769
250 eThrGluGluGlnLysProPheProCysThrGluCysGlyGluIlePheS 267
770 GATCAGAGAGATCTCTCGTGTGTCAGACA.....798
267 erAsnGluHisGluLeuLeuThrHisGlnSerThrHisThrGluGluGln 283
799 .....CTAGCAAGTATGTCGCCAA 818
284 LysProPheProCysThrLysCysTrpGlyIlePheSerAsnGluHisGl 300
819 ACGTAAGAGACTCTATGCTCAGAAATTTCTGGGGACAAAGGCGCTGTCCG 868
300 uLeuArgThrHisGlnSerThrHisThrGluGlyGlnLysSerLeuProS 317
869 ACAGCCCTACGACAGTCCACGTACGAGAGAGAGACGAAATGATG...915
317 erThrGlu...SerGlyGlyThrPheSerAsnGluHisGluLeuLeuThr 332
916 .....AAGTCCCACGTGATGGACCAA.....936
333 HisGlnSerThrHisThrGluGluGlnLysHisLeuProCysThrGluCy 349
937 .....GCCATCAACAGCCATCACTACCTGGGGCGGAGTCCCTGCG 979
349 sGlyClyThrPheThrAsnGluGlnGluLeuLeuAlaHisGlnSerThrH 366
980 GCCCGCTGGTGACAGACGCCCGCGGCGGTTCGAGGTGGTCCCGGTGTCATC 1029
366 isThrGluGluGlnLysProLeuProCysThrGluCysGlyGluIlePhe 382
1030 AGCCCGATGTACAGCTG.....CACAGGGCTCGGAGGCGCCCGCGG 1073

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Percent Similarity: 47.455 Percent Identity: 23.636

alignment_block:
US-08-711-417C-165 x I48689 ..

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40	GGGAGGAAAGCCCCCCTGTAGCGATATCCAGATGAGGGCGATGACGC	89
158	GlyGluAspSerLeuSerThrArgValProGlnLeuAspIleSe	174
90	CATGCCGATCCCCGAGGACCTTCACCACCTCGGAGGACGAGAAGCT	139
174	rSerSerIleArgProSerAspCysLysThrPheGlyAsnLeuGluH	191
140	CAAAGAGTGACAGACTCGTGGCCAGTAATGTTAAGTAGACACTCAGAGT	189
191	isAsnSerGlnLeuValThrGlnSerAsnIleLeuAlaLysLysPro	207
190	GATGAAGAAGAATGGCGCTGCCTGTCAATGAATGGGAAGAATGCGGA	239
208	TyrLys.....Cys.....AspLysCysArgLy	215
240	GAATTATA.....CGAATGCTTGATCGCTCGGAGAGAAAATG.....	276
215	sSerPheIleHisArgSerLeuAsnLysHisGlnLysIleHisLysG	232
277AATGGCTCCACAGGACCGACGAGCGAGCTCGGCTTGG	312
232	LysProTyrSerAsnGlyThr.....AspGlnGly.....AlaGln	244
313	TCGGGAGTTGGAGCATTCGACTTCCTAACCGGAAAACTAAAGTGTGATAT	362
245	SerGly.....ArgLysHisGluCysAlaAs	254
363	CRGTGGGATCATTTGCATCGGCCCCAATGTGCTCATGTTCACAAAAGAA	412
254	pCysGlyLysThrPheLeuTrpArgThrGlnLeuThrGluHisGlnArgI	271
413	GCACACATGGAGACGGCCCTCCAGTCCAATCAGTGGGGCGCTCATTC	462
271	IeHisThrGlyLysProPheGluCysAsnValCysGlyLysAlaPhe	287
463	ACCCAGAGGCAACCTGCTCGCGCACATCAAGTGCATTCCTCGGGGAGAA	512
288	ArgHisSerSerLeuGlyGlnHisGluAsnAlaHisThrGlyGlyLys	304
513	GCCTTCAATGCCACCTCTGCAACTAGCCCTGCGCGGAGGAGGACGCC	562
304	sProTyrGlnCysSerLeuCysGlyLysAlaPheGlnArgSerSerL	321
563	TCATGGCCACCTGAGGACGACCTCCGTTGTTAAACCTCACAAATGTGA	612
321	euaGlnHisGlnArgIleHisThrGlyLysProTyrArgCysAsn	337
613	TATTTGGCCGAGCATATAACAGCGAACGCTCTTTAGAGGAACAATAAGA	662
338	LeuCysGlyArgSerPheArgHisSerThrSerLeuThrGlnHis.....	352
663	GGCTGCCACAACACTACTTGTGAAGCATGGGCTTCCTCGGGCACACTGTACC	712
352	352
713	CAGTCATTAAAGAGAACTAAGCACAGTGAATGGCAGAGACCTGTGC	762
353GluValThrHisSerGlyLysProPheGlnCys	364
763	AAGATAGGATCAGAGATCTCTGCTGTCGACAGACTAGCAAGTATGT	812
365	Lys.....GluCysGlyLysAlaPheSerArgCysSerSerLeuVa	378
813	CGCCAAACGTAAAGAGCTCTATGCCTCAGAAATTTCTTGGGACAAAG....	858

seq_name: pir2:I48689
seq_documentation_block:
gene NK10 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C:Accession: I48689; S49078
R:Lange, R.; Christoph, A.; Thiesen, H.J.; Vopper, G.; Johnson, K.R.; Lemaire, L.; Plomaz
DNA Cell Biol. 14, 971-981, 1995
A>Title: Developmentally regulated mouse gene NK10 encodes a zInc Finger Repressor Prot
A:Reference number: I48689; MUID:96069544
A:Accession: I48689
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-636 <RES>
A:Cross-references: EMBL:X79828; NID:g506501; PIDN:CAA56225.1; PID:g506502
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

alignment_scores:
Quality: 311.00 Length: 550
Ratio: 1.192 Gaps:

378 lGlnHisGluArgThr.....HisThrGlyGluLysProp 390
859GGCTGTCCGACACGCCCTAC 879
390 heGluCysSerIleCysGlyArgAlaPheGlyGlnSerProSerLeuTyr 406
880 GACAGTGCACCTACGAGAGGAGACGAAATGATGAAGTCCACGCTGAT 929
407 LysHisMetArgIleHisLysArgSerLysProTyrGlnSerAsn..... 421
930 GGACCAAGCCATCAACAACGCCATCACTACCTGGGGCCGAGTCCCTGC 979
422AsnPhe.....SerLeuA 426
980 GCCCGTGTGCAGAGCC...CGGGGGTTCGAGGTGTCCTCCGGTC 1026
426 laPheValProAsnThrProLeuProGlnGlyGluLeuLeuThrGlu 442
1027 ATCAGCCCGATG..... 1038
443 ValLysSerTyrHisCysAsnAspCysGlyLysAspPheGlyHisIleTh 459
1039TACCAGTGCACAGCGCTCGGAGGCCACCGCGCTCCACCACT 1084
459 rAspPheSerGluHisGlnArgLeu.....HisA 469
1085 CGGCCAGGACAGCGCGGTGGAGTACCTGCTGCTCTCCAGGCCAAG 1134
469 laGlyGluAsnSerTyrGlySerGluGlnThrLeuLeuGlyGlnSer 485
1135 TTGGTCCCTCGGAGCGCGGTGGAGTCCCGAGCAACACAGTGC..... 1176
486 LeuSerHisProArgGluLysProTyrGlnCysAsnValCysGlyLysAl 502
1177CAAGACTCCAGCAGCCAGGAGCAACACAGGAGCGCGCAGCG 1222
502 aPheLysArgSerPheIleGluHisArgIleHisThrGlyG 519
1223 GTCTTATCTACCTGACCAACCACTCGCCGCGAGCGCGCTCGTGC 1272
519 LuLysProTyrGluCysAsnGluCysGlyGluAlaPheSerArgLeuSer 535
1273 CTCAGGAGGAGGAC.....CGGCCCTAGACCT 1301
536 SerLeuThrGlnHisGluArgThrHisThrGlyGluLysProTyrGluCy 552
1302 GCTG.....CGGCCGCTCCGAGAACTCGCAGGACGCGCTCCGG 1342
552 sIleAspCysGlyLysAlaPheSerGlnSerSerLeuIleGlnHisG 569
1343 TGCTACGACCAAGCGGGAGCAGATGAAGGTGATCAAGTGCAGACCTGC 1392
569 luArgThrHisThrGlyGlu.....LysProTyrGluCysAsnGluCys 583
1393 CGGGTCTCTTCGTGATCAGTCATGTCATGTCACCATCCACATGGGTGCCA 1442
584 GlyArgAlaPheArgLysLysThrAsnLeuHisAspHisGlnArgThrHi 600
1443 CGGCTTCGTGATCCCTTTGAGTGCAACATGTCGGCTACCAACAGG 1492
600 sThrGlyGluLysProTyrAlaCysLysGluCysGlyArgAsn..... 614
1493 ACCGGTACGAGTTCTCGTCACATCAACCGGAGGAGCAGCGCTCCAC 1542
615PheSerArgSerSerAlaLeuThrLys...HisHisArgValHis 628

seq_name: pir2.S10245

seq_documentation_block:

finger protein, testis - mouse

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 01-Dec-2000

C:Accession: S10245

R.Nelki, D.; Dudley, K.; Cunningham, P.; Akhavan, M.
Nucleic Acids Res. 18, 3655, 1990
A:Title: Cloning and sequencing of a zinc finger cDNA expressed in mouse testis.
A:Reference number: S10245; MUID:90301500
A:Accession: S10245
A:Molecule type: mRNA
A:Residues: 1-411 <NDEL>
A:Cross-references: EMBL:X52533; NID:g53456; PIDN:CAA36769.1; PID:g53457
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C:Keywords: DNA binding; zinc finger

alignment_scores:

Quality:	309.00	Length:	479
Ratio:	1.251	Gaps:	24
Percent Similarity:	51.566	Percent Identity:	24.843

alignment_block:

US-08-711-417C-165 x S10245 ..

Align seg 1/1 to: S10245 from: 1 to: 411

130 CAGCAAGCTCCAGAGTGACAGAGTGGCCAGTAATGTTAAAGTAGA 179
6 GluArgAsnAlaThrSerTyrProThrIleSerCysLeuIleLysValTh 22
180 GACTCAGAGTCATGACAGAGAAATGGCGTGTGAAATGAATGGGGAAG 229
22 rLysThrLysProAlaLysAsnValArgLysTyrAlaArgHisSerAlaS 39
230 AATGTGGGAGGATTTACGAATGCTTGATGCCCTCGGGAGAGAAAATGAAT 279
39 erHisThrLysGluAspLysIle.....GlnThrGlyGluLysArgLys 53
280 GGCTCCACAGGAGGACCAAGCGCTGGCTTGTGGGAGTTGGAGGCAT 329
54 ...SerHisCysArgThrProSerLysProGluLysAlaProGly..... 67
330 TCGACTTCCTAACGGAAAA...CTAAAGTGTGATATCTGTGGATCATTT 376
68SerGlyLysProTyrGluCysAsnHisCysGlyLysVal 81
377 GCATCGGGCCCAATGCTCATGTTTCACAAAAGAACGACACTGGAGAA 426
81 euSerHisLysGlnGlyLeuLeuAspHisGlnArgThrHisThrGlyGlu 97
427 CGGCCCTTCAGTCAATCAGTGGGGCCCTCATTCACCCAGAGAGGCA 476
98 LysProTyrGluCysAsnGluCysGlyLeAlaPheSerGlnLysSerHi 114
477 CCGTCTCCGCGACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCC 526
114 sLeuValLeuHisGlnArgThrHisThrGlyGluLysProTyrGluCysG 131
527 ACCTCTCAACTAGCCCTCGCCGGGAGGACGCCCTCACTGGCCACCTG 576
131 luGlnCysGlyLysAlaHisGlyHisLysHisAlaLeuThrAspHisLeu 147
577 AGGACGCACTCCGTTGGTAAACCTCAAAATGTGATATTTGGCCGGAAG 626
148 ArgIleHisThrGlyGluLysProTyrLysCysAsnGluCysGlyLysTh 164
627 CTATTAACAGCAAGCTCTTTAGAGGAACATAAAGAGCGCTGCCCAACT 676
164 rPheArgHisSerSerAsnLeuMetGlnHisLeu...ArgSerHis...Thr 179
677 ACTTGGAAAGCATGGGCCCTTCGGGGACACTGTACCAGTCATTAAAGAA 726
180 GlyGluLysProTyrGluCysLys...GluCysGlyLysSerPheArgTy 195
727 GAAATTAAGCAGCAGTAAATGGCAGAGAACCTGTGTCAAGTAGATC... 773
195 rAsnSerSerLeuThrGluHisValArgThrHisThr...GlyGluIlePro 211

774 AGAGAGATCTCTCGTCTGGCAGACAGTACGAAGTAATGTGCGCAAAACGTA 823
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 212 TyrGluCysAsnGluCysGlyLysAlaPheLys..... 222
 824 AGAGCTCTATGCTCAGAAATTTCTTGGGACAGAGGCTGTCCGACACG 873
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 223TyrGlySerSerLeuThr..... 228
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 924 CGTGATGGACCAAGC..... 946
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 244 GluCysGlyLysThrPheSerLysLysSerHisLeuValIleHisGlnAr 260
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 947 AGCCCATCAACTACCTGGGGGGCGAGTCCCTCGCGCGCTGTGTGCAGAG 996
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 260 gThrHis..... 272
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 997 CCCCCGGCGTCCGAGGTGTCGCGGTATCATCAGCCGATGTACCACT 1046
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 272 LucysGlyLys.....AlaPheGlyHis.SerSerSerLeuThrTy 285
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 1047 GCACAGGCGCTCGGAGGGACCCCGCGCTCCAAACCACTGGGCCCGAGACA 1096
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 285 rHisMetArgThr.....HisThrGlyAsp.... 293
 1097 GCGCCGTGGATACCTGTGCTGCTCTCCAGGCCAAGTGTGTGCGCCCTCG 1146
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 297 Glu.....CysAsnGlnCysGlyLysAlaPhe..... 305
 1197 GAGCAACAGAGGACGACGCGGTCTTATCTACCTGACCAACACCA 1246
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 315GlnArgValHisThrGlyGlu.....LysProPhe 324
 1297 GACTGTGTCGCGCCCTCCGAGAACTCCGAGGAGCGCTCCGGGTGT 1346
 : : : : : : : : : : : ||| : : : : :
 325 GluCysValGluCysGlyLysAlaPheSerGlnLysSerHisLeuIleVa 341
 1347 C.....AGCACAGCGGGGAGCAGATGAAGGTGTACAAGTGGGAAC 1387
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 341 lHisGlnArgThrHisThrGlyGlu.....LysProPheGluCysTyrg 356
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seq_name: pir2:S26823

seq_documentation_block:

zinc finger protein ZNF43 - human

N:Alternate names: zinc finger protein kox27

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 01-Dec-2000

C:Accession: S26823; 137967; S10416

R:Lovering, R.; Trowsdale, J.
 Nucleic Acids Res. 19, 2921-2928, 1991
 A:Title: A gene encoding 22 highly related zinc fingers is expressed in lymphoid cell
 A:Reference number: S26823; MUID:91279444
 A:Accession: S26823
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-803 <LOV>
 A:Cross-references: EMBL:X59244; NID:g38031; PIDN:CAA41932.1; PID:g38032
 R:Thiesen, H.J.
 New Biol. 2, 363-374, 1990
 A:Title: Multiple genes encoding zinc finger domains are expressed in human T cells.
 A:Reference number: I37949; MUID:91145339
 A:Accession: I37967
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 476-531 <THI>
 A:Cross-references: EMBL:X52358; NID:g34160; PIDN:CAA36584.1; PID:g930090
 C:Genetics:
 A:Gene: GDB:ZNF43; HTF6
 A:Cross-references: GDB:128653
 A:Map position: 19p13.1-19p12
 C:Superfamily: zinc finger protein 2FP-36; LIM metal-binding repeat homology
 C:Keywords: DNA binding; zinc finger

alignment_scores:

Quality: 308.00 Length: 405
 Ratio: 1.439 Gaps: 12
 Percent Similarity: 52.840 Percent Identity: 23.704

alignment_block:

US-08-711-417C-165 x S26823 ..

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 402 TCACAAAAGAACCCACTGGAGAACCGCTCCAGTGCATCAATCAGTGGC 451
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 325 sHisArgIleHisThrGlyGluLysProTyThrCysGluCysG 342
 452 GGGCTCATTCACCCAGGGAACCTGCTCCGGCAGCATCAAGCTCAT 501
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 342 lLysAlaPheAsnGlnPheSerAsnLeuThrHisLysArgIleHis 358
 502 TCCGGGAGAGCCCTTCAATGCCACCTCTGCAACTAGCGCTGCCCGC 551
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 359 ThrAlaGluLysPheTyThrLysCysThrGluCysGlyGluAlaPheSerAr 375
 552 GAGGACGCGCTCCTACCTGGCCACCTGAGGACGACCTCCGTTGGTAAACCTC 601
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 375 gSerSerAsnLeuThrLysHisLysIleHisThrGluLysLysProt 392
 602 ACAATGTGATATTGCGCCGAGCTATAACACGACGACGCTCTTTAGAG 651
 : : : : : : : : : : : ||| : : : : :
 392 yrLysCysGluCysGlyLysAlaPheLysTrpSerSerLysLeuThr 408
 652 GAACATAAA.....GAGCGCTGCCCAACTA 677
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 409 GluHisLysLeuThrHisThrGlyGluLysProTyThrLysCysGluLucy 425
 678 CTGGAAAGCATGGCGCTTCGGGACACACTGATCCACGATCAATAAGAG 727
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 425 sGlyLysAlaPheAsnTrpProSerThrLeu..... 435
 728 AAATAACACAGTGAATGGCAGAGAC.....CTGTGCAAG 765
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 436 ..ThrLysHisAsnArgIleHisThrGlyGluLysProTyThrLysCysGlu 451
 766 ATAGGATCAGAGATCTCTCGTGTGGACAGACTAGCAAGTAATGTGCGC 815


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966 GGCGAGTCCCTCGGCGCGTGTGTGTCAGACGCGCGCGGGTTCGAGG 1015
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383 rHisLeuThrThrHisLysIleHisThrGlyGlu..... 395
1016 TGGTCCCGGTTCATCAGCCCGATACCATGTCACAGGCGCTCGGAGGGC 1065
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396 .....LysProTyrLysCysLysGluCys 403
1066 ACCCGCGCTCCAAACCACTCGGCGCCAGGACGCGCGGTGGATCTGCT 1115
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404 GlyLysAlaPheLysHisSer..... 411
1116 CTGCTCTCCAAAGCCCAAGTGTGTGCTCGGAGCGCGGCGTCCCGCA 1165
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412 .ThrLeuThrLysHisLysIleHisThrGlyGluLysProTyrLys 428
1166 GCAACAGCTGCCAAGACTCCACGAGCACACGAGACCAACAGGAGCAG 1215
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
428 erLysGluCysGluLysAlaPheAsnGlnSerSerLys..... 440
1216 CGCAGCGGTCTTATCTACCTGACCAACCAACATCGCCGAGCGCGCA 1265
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
441 .....LeuThrGluHis.....LysLys 446
1266 CGTCTCGCTCAAGGAGGAGCACCGCGCTACGACCTGCTCGCGCGCCT 1315
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
446 sIleHisThrGlyGluLysProTyrGluCysGluLysCysGlyLysAla 463
1316 CCGAGAAGTGGCAGGAGCGCTCGCGTGTGTGTCAGCACCGCGGGAGC 1365
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
463 heAsnGlnSerSerAsnLeuThrArgHisLysLysSerHisThrGlu 479
1366 ATGAAGTGTACAAAGTCGCAACTGCGCGGTGCTCTTCCTGATCAGCT 1415
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
480 ..LysProTyrLysCysGluGluCysGlyLysGlyPheLysTrpPro 495
1416 CATGTACACCATCACATGGCTGGCTGCCAGCGCTTCCTGATGTCAGT 1465
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
495 rThrLeuThrIleHisLysIleHisThrGlyGluLysProTyrLysC 512
1466 GCAACATGTGCGGTACACAGCGGACGAGCGGTACGAGTTCCTGTCGC 1515
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
512 ysgGluGluCysGly.....LysAlaPheAsnGlnSerSerLys 534
1516 ATACGCGCA 1524
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
525 LeuThrLys 527

```

seq_name: pir2:S35305

```

seq_documentation_block:
zinc finger protein ZNF91 - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 05-Nov-1999
C:Accession: S35305
R:Belletroid, E.J.; Marine, J.C.; Ried, T.; Lecocq, P.J.; Riviere, M.; Amemiya, C.; Ponc
EMBO J. 12, 1363-1374, 1993
A:Title: Clustered organization of homologous KRAB zinc-finger genes with enhanced expre
A:Reference number: S35305; MUID:93223677
A:Accession: S35305
A:Molecule type: mRNA
A:Residues: 1-1191 <BE>
A:Cross-references: EMBL:L11672; NID:gl86773; PIDN:AA59469.1; PID:gl86774
A:Note: the authors translated the codon GCA for residue 750 as Thr and GCT for residue
C:Genetics:
A:Gene: GDB:ZNF91; HPF7: HTF10
A:Cross-references: GDB:13284
A:Map position: 19p12-19p12
C:Keywords: DNA binding; zinc finger

alignment_scores:

```

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Quality: 305.50      Length: 491
Ratio: 1.252      Gaps: 16
Percent Similarity: 49.695      Percent Identity: 23.218

alignment_block:
US-08-711-417c-165 x S35305      ..
Align seg 1/1 to: S35305 from: 1 to: 1191

226 GAAGAAATGTGGGAGGATTAGGAATGCTTGCCTCGGAGAGAAAAT 275
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
577 GluGluCys.....GlyLysAlaPh 583

276 GAATGGCTCCACACGAGGACGAGCGCTTGTGCGGAGTTGGAG 325
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
583 easn.....HisSerSerSerLeuSerThrHisLysI 594

326 GCATTTCGACTTCTTAACGGAACCTAAAGTGTGATATCTGTGGATCAT 375
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
594 lIleHisThrGlyGluLysSerTyrLysCysGluGluCysGlyLysAla 610

376 TGCATCGGCGCCCAATGCTCATGCTTCCAAAAGAACCCACACTGGAGA 425
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
611 PheLeuTrpSerSerThrLeuArgArgHisLysArgIleHisThrGlyG 627

426 ACGGCGCTCCAGTGCATCAGTGGCGGCGCTCATTCACCCAGAGGCA 475
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
627 uLysProTyrLysCysGluGluCysGlyLysAlaPheSerHisSerSerA 644

476 ACCTGCTCGGACATCAAGCTGATCCGGGGAGAGCCCTTCAAATGC 525
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
644 lAlaAlaLysHisLysArgIleHisThrGlyGluLysProTyrLysCys 660

526 CACCTCTGCACTACGCTCGCGCGGAGGAGCGCCCTACTGCCACCT 575
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
661 LysGluCysGlyLysAlaPheSerAsnSerSerThrLeuAlaAsnHisL 677

576 GAGGAGCGCACTCCGTGTGTAACCTCACAAATGTGATATTGTGGCCGA 625
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
677 sIleThrHisThrGluGluLysProTyrLysCysLysGluCysAspLys 694

626 GCTATAAACAGCGAAGCTCTTTAGAGGAACATAAA..... 660
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
694 hrPheLysArgLeuSerThrLeuThrLysHisLysIleIleHisAlaGly 710

661 .....GAGCGCTGC..... 669
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
711 GluLysLeuTyrLysCysGluGluCysGlyLysAlaPheAsnArgSerSe 727

670 .....CACAACTACTTGGAAAGCATGGGCTCCG..... 699
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
727 rAsnLeuThrIleHisLysPheIleHisThrGlyGluLysProTyrLysC 744

700 .....GGCACTGTACCCAGTCATTAAAGAAAGAACTAAGCAC 738
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
744 ysGluGluCysGlyLysAlaPheAsnTrpSerSerSerLeuThrLysHis 760

739 AGTGAAGT.....GCAGAAGACCTGTCCCAAGATAGGATCAGA 776
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
761 LysArgIleHisThrArgGluLysProPheLysCysLysGluCysGlyL 777

777 GAGATCTCTGCTGGACAGACTAGCAAGTAATGTCGCCAAACGTAAGA 826
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
777 salaPheIleTrpSerSerThrLeuThrArgHisLysArgIleHisThrG 794

827 GCTCTATGCTCAGAAATTTCTTGGGGAGAGCGCTGTCCGACACGCC 876
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
794 lyGluLysProTyrLys...CysGluGluCysGlyLysAlaPheSerArg 809
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
877 TAGCAGAGTCCACCTACGAGAGGAGAACGAATGATGAAGTCCACGT 926
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
810 SerSerThrLeuThrLysHisLysThrIleHisThrGlyGluLysProTy 826

```

```
927 GATGACCAAGCCATCAACACGACATCACTACCTGCGGCCGAGTCCC 976
    :::::::::::::::::::::
826 rLysCysGluCysGlyLysAlaPheLysHisSerSerAlaLeuAlaL 843
977 TGCCTCCGCTGGTGCACAGCCGCCCGGGCGGTTCAGAGTGTCCCGGTC 1026
    :::::::::::::::::::::
843 ySHisLysIleIleHisAlaGlyGlu..... 851
1027 ATCAGCCCGATGTACCACTGCACAGCGCTCGAGGCGCACCCGCGCTC 1076
    :::::::::::::::::::::
852 .....LysLeuTyrLysCysGluGluCysGlyLysAlaPhe 863
1077 CAACACTCGCCCGCAGACAGCGCGGTGGAGTACCTGCTGCTCTCCCA 1126
    :::::::::::::::::::::
863 eAsnGlnSerSerAsn.....LeuThrT 871
1127 AGGCCAAGTGGTCCCTCGAGCGCGAGCGTCCCGGACACAGCTGC 1176
    :::::::::::::::::::::
871 hrHisLysIleIleHisThrLysGluLysProSerLysSerGluGluCys 887
1177 CAA.....GACTCCAGCAGCACCGAGACGACACACAGGAGGA 1211
    :::::::::::::::::::::
888 AspLysAlaPheIleTrpSerSerThrLeuThrGluHisLysArgIleH 904
1212 GCAGCGC.....AGCG 1222
    :::::::::::::::::::::
904 sThrArgGluLysProTyrLysCysGluGluCysGlyLysAlaPheSerG 921
1223 GTCTATCTACCTGACCAACACACATCCCGCAGCGCGCGAGCGGTGTCG 1272
    :::::::::::::::::::::
921 lnProSerHisLeuThrThrHis.....LysArgMetHis 932
1273 CTCAGGAGGAG...CACCGCGCTACGACCTGCTGCGCGCGCGCTCCGA 1319
    :::::::::::::::::::::
933 ThrGlyGluLysProTyrLysCysGluGluCysGlyLysAlaPheSerG 949
1320 GAACCTCGACGAGCGCTCGCGGTGTCACACACGCGGCGGAGCAGATGA 1369
    :::::::::::::::::::::
949 nSerSerThrLeuThrThrHisLysIleIleHisThrGlyGlu.....L 964
1370 AGGTGTACAAGTCGACACCTGCGGGTGTCTCTCTGATCAGTCATG 1419
    :::::::::::::::::::::
964 ysProTyrLysCysGluGluCysGlyLysAlaPheArgLysSerSerThr 980
1420 TACACCATCCACATGGCTCCCGCGGTCTCCGTCATCTTTTGGATGCAA 1469
    :::::::::::::::::::::
981 LeuThrGluHisLysIleIleHisThrGlyGluLysProTyrLysCysG 997
1470 CATGTGCGGTACACACGACGCGGTACGAGTCTCTGTCGACACATAA 1519
    :::::::::::::::::::::
997 uGluCysGly.....LysAlaPheSerGlnSerSerThrLeuT 1010
1520 CGCGAGGGGAGCACCGCTTCCAC 1542
    :::::::::::::::::::::
1010 hrArg....HisThrArgMetHis 1016
```

seq_name: pir2:JH0500

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seq_documentation_block:
zinc finger protein 29 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Dec-2000
C:Accession: JH0500
R:Denny, P.; Ashworth, A.
Gene 106, 221-227, 1991
A:Title: A zinc finger protein-encoding gene expressed in the post-meiotic phase of sper
A:Reference number: JH0500; MUID:92039080
A:Accession: JH0500
A:Molecule type: mRNA
A:Residues: 1-614 <DEN>
A:Cross-references: GB:X55126; NID:955470; PIDN:CAA38920.1; PID:955471
A:Experimental source: testis
C:Keywords: DNA binding; zinc finger
```

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F:217-244/Region: zinc finger
F:245-272/Region: zinc finger
F:273-300/Region: zinc finger
F:301-328/Region: zinc finger
F:329-356/Region: zinc finger
F:357-384/Region: zinc finger
F:385-412/Region: zinc finger
F:413-440/Region: zinc finger
F:441-468/Region: zinc finger
F:469-496/Region: zinc finger
F:497-524/Region: zinc finger
F:525-552/Region: zinc finger
F:553-580/Region: zinc finger
F:581-608/Region: zinc finger

alignment_scores:
  Quality: 305.00      Length: 649
  Ratio: 1.105        Gaps: 26
  Percent Similarity: 42.527      Percent Identity: 21.263
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alignment_block:

US-08-711-417C-165 x JH0500 ..

Align seg 1/1 to: JH0500 from: 1 to: 614

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4 GATGCTCAGCAGGTCACAGACATGCTTCTCATCAGGAGGAAAGCCC 53
    |||||: |||||: |||||: |||||: |||||: |||||: |||||:
47 AspGlyProGluSerGluProPheProGlnSerAlaGlyLysGlySerPr 63
    : |||||:
54 CCCTGTGAAGCGATACT..... 69
    : |||||:
63 oGlnGluAspAlaAlaGluGlyProGlnGlyAlaLeuValArgPheA 80
    : |||||:
69 ..... 69
80 rgGluLeuCysArgArgTrpLeuArgProGluValHisThrLysGluGln 96
    ..... 69
97 MetLeuThrValLeuProArgGluIleGlnAlaTrpLeuGlnGluHisAr 113
70 .CCAGATGAGGGGATGAGCCCATGCGCATGCCGAGGACCTCTCCACCA 118
    |||||: |||||: |||||: |||||: |||||: |||||: |||||:
113 gProGluSerSerGluGluAlaValAlaLeuValGluAspLeuThrGlnT 130
    : |||||:
119 CC..... 120
    : |||||:
130 hrPheArgHisSerAspPheGluIleGlnSerGluAsnGlyGluAsnSer 146
    ..... 120
120 ..... 120
147 AsnGluAspMetPheGluGlyValGluSerHisGlyMetPheLeuAsnI 163
121 .TCGGGAGGACAGCAAGTCCCAAGAGTGCACAGAGTCGTGGCCAGTAATG 169
    |||||: |||||: |||||: |||||: |||||: |||||: |||||:
163 eSerGlyGlyGluGlyGlnGlnSerAsp..... 173
170 TTAAGTAGAGACTCAGAGTATGAAGAGAAATGGCGTGCCTGTGAATG 219
    : |||||: |||||: |||||: |||||: |||||: |||||: |||||:
174 .....GlyAspSerAspPheGluArgAspCysGlySer 184
220 AATGGGAAGAA.....TGTGGGAGGATTTACGAATGCTTGTATGC 260
    : |||||: |||||: |||||: |||||: |||||: |||||: |||||:
185 GlyGlyAlaGlnGlyHisAlaProGlyGluAspProArgValValProSe 201
261 CTGGGAGAGAAATGAATGGCTCCACAGGACAGGACAGGCGCTCGCCTT 310
    : |||||: |||||: |||||: |||||: |||||: |||||: |||||:
201 rGluGlyArgGluVal.....GlyGlnL 209
311 TGTGGGAGTGGAGTTCGACTTCCTTAACGAGAACTAAAGTGTGAT 360
    : |||||: |||||: |||||: |||||: |||||: |||||: |||||:
209 eulGlyLeuGlnGlyThrTyrLeuGlyGluLysProTyrGluCysPro 225
```

```

361 ATCTGTGGATCATTTGCATCGCGGCCCAANGTCTCATGTTCACAAAAG 410
|||||
226 GlnCysGlyLysThrPheSerArgLysSerHisLeuIleThrHisGluAr 242
|||||
411 A..... 411
242 gThrHisThrGlyGluLysTyrTyrLysCysAspGluCysGlyLysSerP 259
412 .....AGCCACACTGGAGAA 426
259 heSerAspGlySerAsnPheSerArgHisGlnThrThrHisThrGlyGlu 275
427 CGGCCCTTCAGTGCATCATGTCGGGGCCTCATTCACCCAGAAGGCCAA 476
|||||
276 LysProTyrLysCysArgAspCysGlyLysSerPheSerArgSerAlaAs 292
477 CTTGCTCCGGCACAATCAAGTCTCCGGGAGAAAGCCCTTCAAAATGCC 526
|||||
292 nLeuIleThrHisGlnArgIleHisThrGlyGluLysProPheGlnCysA 309
527 ACCTGTGCAACTACGCTCGCCGCGGAGGACGCCCTCACTGGCCACCTG 576
|||||
309 laGluCysGlyLysSerPheSerArgSerProAsnLeuIleAlaHisGln 325
577 AGGACGCACTCCGTTGGTAAACCTCAAAATGGATATGTGGCCGAAG 626
|||||
326 ArgThrHisThrGlyGluLysProTyrSerCysProGluCysGlyLysSe 342
627 CTATAAAGCAGCAAGCTCTTTAGAGAAACATAAAGAGCGCTGCCACAAC 676
|||||
342 rPheGlyAsnArgSerSerLeuAsnThrHis...GlnGlyIleHis.Thr 357
677 ACTTGGAAACATGGCCCTTCGGGCACACTGTACCCAGTCAATTAAGAA 726
|||||
358 GlyGluLysProTyrAlaCysLys...GluCysGlyLysSerPheSerty 373
727 GAACTAAGCAGACATGAATGGCAGAAAGACCTGTGCAAGATAGGATCAGA 776
|||||
373 rAsnSerAsnLeuIleArgHisGlnArgIleHisThr.....GlyGluL 388
777 GAGATCTCTCGTCTGGACAGACTAGCAAGTAATGTCGCGCAAGGTAAGA 826
388 ysProTyrLysCys..... 392
827 GCTCTATGCTCAGAAATTTCTTGGGACAAAGGCGCTGTCCGACACGCC 876
|||||
393 ThrGluCysGlyGlnLysPheSerGlnSerSerAlaLeu..... 405
877 TAGCAGAGTCCACGTACGAGAGGAGAGCAAGAAATGATGAATCCACGT 926
406 .....IleThrHisArgArgThr..... 411
927 GATGGACCAAGCCATCAACAAGCCCATCAACTACCTGGGGCGGAGTCCC 976
412 .....HisThrGlyGluLysProTyrGln 419
977 TGGCCCGCTGTGGAGAGCCCGCGGGCGGTCCGAGGTGTCCCGTTC 1026
|||||
420 CysGlyGlu...CysGlyLys.....AsnPheSerArgSe 430
1027 ATCA.....GCC 1034
430 rSerAsnLeuAlaThrHisArgThrHisLeuValGluLysProTyrL 447
1035 GATGTACCAAGCTGC.....ACAGCGCTCGGAGGCA 1066
447 yscysGlyLeuCysGlyLysSerPheSerGlnSerSerLeuIleAla 463
1067 CCCCAGCTCCAAACCACTCGGCCAGGACAGCGCGGTGAGTACCTGCTG 1116
464 HisGlnGlyThrHisThrGlyGluLys.....ProTyrGluCysLeuTh 478

```

```

1117 CTGCTCTCAAAGGCCAAGTTGGTGCCTTCGAGCGCGAGCGTCCCGAG 1166
|||||
478 tcysgylgluserpheSerTrpSerSerAsnLeuIleLysHisGlnArgT 495
1167 CA...ACAGCTCCCAAGACTCCACGGACACGAGAGCAACACGAGGAGC 1213
495 hrHisThrGlyGluLysProTyrArgCys.GlyAspCysGlyLysGlyPh 511
1214 AGCGAGCGGTCTTATCTACCTGACCAACACCATCATCGCCGCGCGCAA 1263
511 eSerGlnArgSerGlnLeu.....ValValHisGlnArgThrHisThr. 525
1264 CGCTGTCTCAAGGAGGAGACCGCCCTACGACCTGTCTGCGCGCGC 1313
526 .....Gly.GluLysProTyrLysCysLeuMetCysG 536
1314 CTCGAGAACTCGCAGGAGCGCTCCGGGTGTC.....AGCACCA 1354
536 yLysSerPheSerArgGlySerIleLeuValMetHisGlnArgAlaHisL 553
1355 CGCGGAGCAGATGAAGGTGTACAAGTGCAGAACACTGCCGGGTCTCTTC 1404
553 euGlyAsp.....LysProTyrArgCysProGluCysGlyLysGlyPhe 567
1405 CTGATCATCATGTACACCATCCACATGGCTGCCACGCTTCCGTGA 1454
568 SerTrpAsnSerValLeuIleIleHisGlnArgIleHisThrGlyGly 584
1455 TCCTTTTGAGTCAACATGTGCGGTACACACGACGAGCGGTACGAGT 1504
584 sProTyrArgCysProGluCysGlyLysGlyPheSerAsnSerSerAsn 601
1505 TCTCTGCACATAACGCGGAGGAGCACCGCTTCCACATG 1545
601 heIleThrHis.....GlnArgThrHisLeu 609

```

seq_name: pir2:A38073

seq_documentation_block:

N;Transcription activator ZNF35 - human

A;Alternate names: finger protein HF.10; zinc finger protein 35

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Dec-2000

C;Accession: A38073; S00753

R;Lanfranccone, L.; Pengue, G.; Pandolfi, P.P.; Salcini, A.E.; Giacomucci, A.; Longo,

Genomics 12, 720-728, 1992

A;Title: Structural and functional organization of the HF.10 human zinc finger gene (

A;Reference number: A38073; MUID:92241871

A;Accession: A38073

A;Molecule type: DNA

A;Residues: 1-519 <LAN>

A;Cross-references: GB:I35269; NID:g1162931; PIDN:AAA85451.1; PID:g1162933

A;Note: sequence extracted from NCBI backbone (NCBIN:98395, NCBIN:98399, NCBIN:98401,

R;Pannuti, A.; Lanfranccone, L.; Pascucci, A.; Pelicci, P.G.; La Mantia, G.; Lania, L.

Nucleic Acids Res. 16, 4227-4237, 1988

A;Title: Isolation of cDNAs encoding finger proteins and measurement of the correspon

A;Reference number: S00753; MUID:88247738

A;Accession: S00753

A;Molecule type: mRNA

A;Residues: 1-404,433-519 <PAN>

A;Cross-references: EMBL:X07289; NID:g32070; PIDN:CAA30268.1; PID:g32071

C;Genetics:

A;Gene: GDB:ZNF35

A;Cross-references: GDB:120507; OMIM:194533

A;Map position: 3p21-3p21

C;Introns: 56/3; 105/1

C;Superfamily: zinc finger protein 2FP-36; LIM metal-binding repeat homology

C;Keywords: DNA binding; transcription regulation; zinc finger

alignment_scores:

Quality: 304.50

Length: 528

Ratio: 1.296

Gaps: 20

